PF-0114 US

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
Au-Young, Janice
Goli, Surya K.
Hillman, Jennifer L.

(ii) TITLE OF THE INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: U.S.
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0114 US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
 1               5                  10                  15
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
            20                  25                  30
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
        35                  40                  45
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
    50                  55                  60
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
65                  70                  75                  80
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
                85                  90                  95
Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
            100                 105                 110
Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
        115                 120                 125
Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
    130                 135                 140
Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
145                 150                 155                 160
Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala
                165                 170                 175
Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
            180                 185                 190
Gly Leu Lys Arg Lys Ala Glu
        195
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
- (A) LIBRARY:
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GGTTTGTGCA GTTACAGCTT TTCTNTTGGT ATGCATAATT AATANTTGGA GCTGCAAAGA     60
GATCGTGACA AGAGATGGAC GGTCAGAAGA AAAATTGGAA GGACAAGGTT GTTGACCTCC    120
TGTACTGGAG AGACATTAAG AAGACTGGAG TGGTGTTTGG TGCCAGCCTA TTCCTGCTGC    180
TTTCATTGAC AGTATTCAGC ATTGTGAGCG TAACAGCCTA CATTGCCTTG GCCCTGCTCT    240
CTGTGACCAT CAGCTTTAGG ATATACAAGG GTGTGATCCA AGCTATCCAG AAATCAGATG    300
AAGGCCACCC ATTCAGGGCA TATCTGGAAT CTGAAGTTGC TATATCTGAG GAGTTGGTTC    360
AGAAGTACAG TAATTCTGCT CTTGGTCATG TGAACTGCAC GATAAAGGAA CTCAGGCGCC    420
TCTTCTTAGT TGATGATTTA GTTGATTCTC TGAAGTTTGC AGTGTTGATG TGGGTATTTA    480
CCTATGTTGG TGCCTTGTTT AATGGTCTGA CACTACTGAT TTTGGCTCTC ATTTCACTCT    540
TCAGTGTTCC TGTTATTTAT GAACGGCATC AGGCACAGAT AGATCATTAT CTAGGACTTG    600
CAAATAAGAA TGTTAAAGAT GCTATGGCTA AAATCCAAGC AAAAATCCCT GGATTGAAGC    660
GCAAAGCTGA ATGAAAACGC CCAAAATAAT TAGTAGGAGT TCATCTTTAA AGGGGATATT    720
```

CATTTGATTA TACGGGGGAG GGTCAGGGAA GAACGACCTT GACGTTGCAG TGCAGTTTCA 780
CAGATCGTTG TTAGATCTT 799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1NOB01
(B) CLONE: 31870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Glu Arg Xaa Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
1 5 10 15
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
20 25 30
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Val
35 40 45
His Asp Leu Ile Xaa Trp Arg Asp Val Lys Lys Thr Gly Phe Val Phe
50 55 60
Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile
65 70 75 80
Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser
85 90 95
Phe Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu
100 105 110
Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser
115 120 125
Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His Ile Asn Arg
130 135 140
Ala Leu Lys Leu Ile Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp
145 150 155 160
Ser Leu Lys Leu Ala Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala
165 170 175
Val Phe Asn Gly Ile Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Xaa
180 185 190
Ser Val Pro Ile Val Tyr Xaa Lys Tyr Lys Val Pro Ser Lys Thr Pro
195 200 205
Trp Asn Arg Gln Lys Lys Gly Arg Ile Ser Thr Trp Lys Pro Glu Met
210 215 220
Gln Gln Leu Leu Lys His His Leu Ile Val Ile Thr Ser Leu Leu Val
225 230 235 240
Leu

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1095 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1NOB01
(B) CLONE: 31870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ACACNAGCGN NTCGNGCTCC CGAACCTCTA GCTGCGACTC GGANTGAGTC AGTCAGTCTG     60
TCGGAGTCTG TCCTCGGAGC AGGCGGAGTA AAGGGACTTG AGCGAGCCAG TTGCCGGATT    120
ATTCTATTTC CCCTCCCTCT CTCCCGCCCC GTATCTCTTT TCATTTTNNT NCCACCCTTG    180
CTCGCGTANC ATGGCGGAGC GTNCGGCGGC CACTCAGTCC CATTCCATCT CCTCGTCGTC    240
CTTCGGAGCC GAGCCGTCCG CGCCCGGCGG CGGCGGGAGC CCAGGAGCCT GCCCCGCCCT    300
GGGGACGAAG AGCTGCAGCT CCTCCTGTGC GGTGCACGAT CTGATTTTMT GGAGAGATGT    360
GAAGAAGACT GGGTTTGTCT TTGGCACCAC GCTGATCATG CTGCTTTCCC TGGCAGCTTT    420
CAGTGTCATC AGTGTGGTTT CTTACCTCAT CCTGGCTCTT CTCTCTGTCA CCATCAGCTT    480
CAGGATCTAC AAGTCCGTCA TCCAAGCTGT ACAGAAGTCA GAAGAAGGCC ATCCATTCAA    540
AGCCTACCTG GACGTAGACA TTACTCTGTC CTCAGAAGCT TTCCATAATT ACATGAATGC    600
TGCCATGGTG CACATCAACA GGGCCCTGAA ACTCATTATT CGTCTCTTTC TGGTAGAAGA    660
TCTGGTTGAC TCCTTGAAGC TGGCTGTCTT CATGTGGCTG ATGACCTATG TTGGTGCTGT    720
TTTTAACGGA ATCACCCTTC TAATTCTTGC TGAACTGCTC ATTTTNAGTG TCCCGATTGT    780
NTATNAGAAG TACAAGGTTC CAAGCAAAAC TCCCTGGAAT CGCCAAAAAA AAGGCAGAAT    840
AAGTACATGG AAACCAGAAA TGCAACAGTT ACTAAAACAC CATTTAATAG TTATAACGTC    900
GTTACTTGTA CTATGAAGGA AAATACTCAG TGTCAGCTTG AGCCTGCATT CCAAGCTTTT    960
TTTTTAATTT GGTGGTTTTC TCCCATCCTT TCCCTTTAAC CCTCAGTNTC AAGCACAAAN   1020
TTTNATGGAC TGATAANNGA TCTATNTTAG ANCTCAGAAG ANGANAGNTT CANNTGCATA   1080
GGNTAAGGNA NTACC                                                    1095
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 776 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 307307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Ala Ala Pro Gly Asp Pro Gln Asp Glu Leu Leu Pro Leu Ala Gly
 1               5                  10                  15
Pro Gly Ser Gln Trp Leu Arg His Arg Gly Glu Gly Glu Asn Glu Ala
            20                  25                  30
Val Thr Pro Lys Gly Ala Thr Pro Ala Pro Gln Ala Gly Glu Pro Ser
        35                  40                  45
Pro Gly Leu Gly Ala Arg Ala Arg Glu Ala Ala Ser Arg Glu Ala Gly
    50                  55                  60
Ser Gly Pro Ala Arg Gln Ser Pro Val Ala Met Glu Thr Ala Ser Thr
65                  70                  75                  80
```

```
Gly Val Ala Gly Val Ser Ser Ala Met Asp His Thr Phe Ser Thr Thr
                85                  90                  95
Ser Lys Asp Gly Glu Gly Ser Cys Tyr Thr Ser Leu Ile Ser Asp Ile
            100                 105                 110
Cys Tyr Pro Pro Gln Glu Asp Ser Thr Tyr Phe Thr Gly Ile Leu Gln
        115                 120                 125
Lys Glu Asn Gly His Val Thr Ile Ser Glu Ser Pro Glu Glu Leu Gly
    130                 135                 140
Thr Pro Gly Pro Ser Leu Pro Asp Val Pro Gly Ile Glu Ser Arg Gly
145                 150                 155                 160
Leu Phe Ser Ser Asp Ser Gly Ile Glu Met Thr Pro Ala Glu Ser Thr
                165                 170                 175
Glu Val Asn Lys Ile Leu Ala Asp Pro Leu Asp Gln Met Lys Ala Glu
            180                 185                 190
Ala Tyr Lys Tyr Ile Asp Ile Thr Arg Pro Glu Glu Val Lys His Gln
        195                 200                 205
Glu Gln His His Pro Glu Leu Glu Asp Lys Asp Leu Asp Phe Lys Asn
    210                 215                 220
Lys Asp Thr Asp Ile Ser Ile Lys Pro Glu Gly Val Arg Glu Pro Asp
225                 230                 235                 240
Lys Pro Ala Pro Val Glu Gly Lys Ile Ile Lys Asp His Leu Leu Glu
                245                 250                 255
Glu Ser Thr Phe Ala Pro Tyr Ile Asp Asp Leu Ser Glu Glu Gln Arg
            260                 265                 270
Arg Ala Pro Gln Ile Thr Thr Pro Val Lys Ile Thr Leu Thr Glu Ile
        275                 280                 285
Glu Pro Ser Val Glu Thr Thr Thr Gln Glu Lys Thr Pro Glu Lys Gln
    290                 295                 300
Asp Ile Cys Leu Lys Pro Ser Pro Asp Thr Val Pro Thr Val Thr Val
305                 310                 315                 320
Ser Glu Pro Glu Asp Asp Ser Pro Gly Ser Ile Thr Pro Pro Ser Ser
                325                 330                 335
Gly Thr Glu Pro Ser Ala Ala Glu Ser Gln Gly Lys Gly Ser Ile Ser
            340                 345                 350
Glu Asp Glu Leu Ile Thr Ala Ile Lys Glu Ala Lys Gly Leu Ser Tyr
        355                 360                 365
Glu Thr Ala Glu Asn Pro Arg Pro Val Gly Gln Leu Ala Asp Arg Pro
    370                 375                 380
Glu Val Lys Ala Arg Ser Gly Pro Pro Thr Ile Pro Ser Pro Leu Asp
385                 390                 395                 400
His Glu Ala Ser Ser Ala Glu Ser Gly Asp Ser Glu Ile Glu Leu Val
                405                 410                 415
Ser Glu Asp Pro Met Ala Ala Glu Asp Ala Leu Pro Ser Gly Tyr Val
            420                 425                 430
Ser Phe Gly His Val Gly Gly Pro Pro Pro Ser Pro Ala Ser Pro Ser
        435                 440                 445
Ile Gln Tyr Ser Ile Leu Arg Glu Glu Arg Glu Ala Glu Leu Asp Ser
    450                 455                 460
Glu Leu Ile Ile Glu Ser Cys Asp Ala Ser Ser Ala Ser Glu Glu Ser
465                 470                 475                 480
Pro Lys Arg Glu Gln Asp Ser Pro Pro Met Lys Pro Ser Ala Leu Asp
                485                 490                 495
Ala Ile Arg Glu Glu Thr Gly Val Arg Ala Glu Glu Arg Ala Pro Ser
            500                 505                 510
Arg Arg Gly Leu Ala Glu Pro Gly Ser Phe Leu Asp Tyr Pro Ser Thr
        515                 520                 525
```

```
Glu Pro Gln Pro Gly Pro Glu Leu Pro Pro Gly Asp Gly Ala Leu Glu
    530                 535                 540
Pro Glu Thr Pro Met Leu Pro Arg Lys Pro Glu Glu Asp Ser Ser Ser
545                 550                 555                 560
Asn Gln Ser Pro Ala Ala Thr Lys Gly Pro Gly Pro Leu Gly Pro Gly
                565                 570                 575
Ala Pro Pro Pro Leu Leu Phe Leu Asn Lys Gln Lys Ala Ile Asp Leu
            580                 585                 590
Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe
        595                 600                 605
Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val
    610                 615                 620
Ala Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile
625                 630                 635                 640
Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro
                645                 650                 655
Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile
            660                 665                 670
Gln Lys Tyr Thr Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr Leu Lys
        675                 680                 685
Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys
    690                 695                 700
Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn
705                 710                 715                 720
Gly Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro
                725                 730                 735
Val Val Tyr Val Lys His Gln Ala Gln Ile Asp Gln Tyr Leu Gly Leu
            740                 745                 750
Val Arg Thr His Ile Asn Ala Val Val Ala Lys Ile Gln Ala Lys Ile
        755                 760                 765
Pro Gly Ala Lys Arg His Ala Glu
    770                 775
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 307309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ala Ala Glu Asp Ala Leu Pro Ser Gly Tyr Val Ser Phe Gly His
 1               5                  10                  15
Val Gly Gly Pro Pro Pro Ser Pro Ala Ser Pro Ser Ile Gln Tyr Ser
            20                  25                  30
Ile Leu Arg Glu Glu Arg Glu Ala Glu Leu Asp Ser Glu Leu Ile Ile
        35                  40                  45
Glu Ser Cys Asp Ala Ser Ser Ala Ser Glu Glu Ser Pro Lys Arg Glu
    50                  55                  60
```

```
Gln Asp Ser Pro Pro Met Lys Pro Ser Ala Leu Asp Ala Ile Arg Glu
65                  70                  75                  80
Glu Thr Gly Val Arg Ala Glu Glu Arg Ala Pro Ser Arg Arg Gly Leu
                85                  90                  95
Ala Glu Pro Gly Ser Phe Leu Asp Tyr Pro Ser Thr Glu Pro Gln Pro
            100                 105                 110
Gly Pro Glu Leu Pro Pro Gly Asp Gly Ala Leu Glu Pro Glu Thr Pro
        115                 120                 125
Met Leu Pro Arg Lys Pro Glu Glu Asp Ser Ser Ser Asn Gln Ser Pro
    130                 135                 140
Ala Ala Thr Lys Gly Pro Gly Pro Leu Gly Pro Gly Ala Pro Pro Pro
145                 150                 155                 160
Leu Leu Phe Leu Asn Lys Gln Lys Ala Ile Asp Leu Leu Tyr Trp Arg
                165                 170                 175
Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe Leu Leu Leu Leu
            180                 185                 190
Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val Ala Tyr Leu Ala
        195                 200                 205
Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val
    210                 215                 220
Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro Phe Lys Ala Tyr
225                 230                 235                 240
Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile Gln Lys Tyr Thr
                245                 250                 255
Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr Leu Lys Glu Leu Arg Arg
            260                 265                 270
Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu
        275                 280                 285
Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu
    290                 295                 300
Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro Val Val Tyr Val
305                 310                 315                 320
Lys His Gln Ala Gln Ile Asp Gln Tyr Leu Gly Leu Val Arg Thr His
                325                 330                 335
Ile Asn Ala Val Val Ala Lys Ile Gln Ala Lys Ile Pro Gly Ala Lys
            340                 345                 350
Arg His Ala Glu
        355
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 208 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
  (A) LIBRARY: GenBank
  (B) CLONE: 307311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Gln Ala Thr Ala Asp Ser Thr Lys Met Asp Cys Val Trp Ser Asn
 1               5                  10                  15
```

```
Trp Lys Ser Gln Ala Ile Asp Leu Leu Tyr Trp Arg Asp Ile Lys Gln
            20                  25                  30
Thr Gly Ile Val Phe Gly Ser Phe Leu Leu Leu Leu Phe Ser Leu Thr
        35                  40                  45
Gln Phe Ser Val Val Ser Val Val Ala Tyr Leu Ala Leu Ala Ala Leu
    50                  55                  60
Ser Ala Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Leu Gln Ala Val
65                  70                  75                  80
Gln Lys Thr Asp Glu Gly His Pro Phe Lys Ala Tyr Leu Glu Leu Glu
                85                  90                  95
Ile Thr Leu Ser Gln Glu Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln
            100                 105                 110
Phe Tyr Val Asn Ser Thr Leu Lys Glu Leu Arg Arg Leu Phe Leu Val
        115                 120                 125
Gln Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Leu Leu
    130                 135                 140
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Leu Met Ala
145                 150                 155                 160
Val Val Ser Met Phe Thr Leu Pro Val Val Tyr Val Lys His Gln Ala
                165                 170                 175
Gln Ile Asp Gln Tyr Leu Gly Leu Val Arg Thr His Ile Asn Ala Val
            180                 185                 190
Val Ala Lys Ile Gln Ala Lys Ile Pro Gly Ala Lys Arg His Ala Glu
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 281046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Asp Cys Val Trp Ser Asn Trp Lys Ser Gln Ala Ile Asp Leu Leu
 1               5                  10                  15
Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe Leu
            20                  25                  30
Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val Ala
        35                  40                  45
Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile Tyr
    50                  55                  60
Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro Phe
65                  70                  75                  80
Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile Gln
                85                  90                  95
Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr Leu Lys Glu
            100                 105                 110
Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys Phe
        115                 120                 125
```

```
Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn Gly
    130                 135                 140
Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro Val
145                 150                 155                 160
Val Tyr Val Lys His Gln Ala Gln Val Asp Gln Tyr Leu Gly Leu Val
                165                 170                 175
Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala Lys Ile Pro
            180                 185                 190
Gly Ala Arg Gly Met Leu Ser Arg Trp Leu Pro Gln Glu Lys Pro Asp
        195                 200                 205
Met Asn Gly Gly Val Trp Ser Gly Asn Ser Ser Leu Leu Pro Arg Tyr
    210                 215                 220
Cys Glu Leu Ile Val Ser Leu Pro Gln Tyr His Asn Leu Arg Gly Lys
225                 230                 235                 240
Leu Arg Asp Arg Cys Phe Gln Ser Phe Pro Val Leu Leu Gly Tyr Leu
                245                 250                 255
Ser Pro Pro Arg Pro Leu Ser Ser Thr Lys Val
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 261 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
  (A) LIBRARY: SPLNFET01
  (B) CLONE: 28742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CCTATNCCNG CTGCTTTCAT TGACAGTATT CAGCATTGTG AGCGTAACAG CCTACATTGC     60
CTTNGCCCTG CNCTCTGTGA CCATCAGCTN TAGGCTATAC AAGGGTGTGA TCCAAGCTAT    120
CCAGAAATCA GATGAAGGNC ACCCATTCAG GGCATATCTG GANTCTGAAG TTGCTATATC    180
TGAGGAGTTG NTTCAGAAGT ACACGTAAAT NNTGNNCNTG GTCAATGTGA NCTCCACGNC    240
TAANGGANCT CAGGTGCCTA T                                              261
```